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Reference

1. Blanquart F, Wymant C, Cornelissen M, Gall A, Bakker M, Bezemer D, et al. (2017) Viral genetic variation accounts for a third of variability in HIV-1 set-point viral load in Europe. PLoS Biol 15(6): e2001855. https://doi.org/10.1371/journal.pbio.2001855 PMID: 28604782